ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/714449

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ___ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ___ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ___ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ___ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ___ Variable Length

Sequence(s) ___ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 ___ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) ___. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 ___ Skipped Sequences (OLD RULES)

Sequence(s) ___ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ___ Skipped Sequences (NEW RULES)

Sequence(s) ___ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ___ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ___ Use of <213>Organism (NEW RULES)

Sequence(s) ___ are missing this mandatory field or its response.

119-119 (and more)

12 ___ Use of <220>Feature (NEW RULES)

Sequence(s) ___ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 ___ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

RAW SEQUENCE LISTING   DATE: 12/01/2000
PATENT APPLICATION: US/09/714,449   TIME: 12:30:04

Input Set : A:\00431PHRM293.txt
Output Set: N:\CRF3\12012000\I714449.raw

```
 3  <110> APPLICANT: Vogeli, Gabriel
 4        Huff, Rita
 5        Sejlitz, Torsten
 6        Lind, Peter
 7        Slightom, Jerry
 8        Schellin, Kathleen
 9        Bannigan, Chris
10        Ruff, Valerie
11        Kaytes, Paul
12        Wood, Linda
13        Parodi, Luis
14        Hiebsch, Ronald
16  <120> TITLE OF INVENTION: Novel G Protein Coupled Receptors
18  <130> FILE REFERENCE: 00431PHRM293
20  <140> CURRENT APPLICATION NUMBER: US/09/714,449
20  <141> CURRENT FILING DATE: 2000-11-16
20  <150> PRIOR APPLICATION NUMBER: 60/165,838
21  <151> PRIOR FILING DATE: 1999-11-16
23  <150> PRIOR APPLICATION NUMBER: 60/198,568
24  <151> PRIOR FILING DATE: 2000-04-20
26  <150> PRIOR APPLICATION NUMBER: 60/166,071
27  <151> PRIOR FILING DATE: 1999-11-17
29  <150> PRIOR APPLICATION NUMBER: 60/166,678
30  <151> PRIOR FILING DATE: 1999-11-19
32  <150> PRIOR APPLICATION NUMBER: 60/173,396
33  <151> PRIOR FILING DATE: 1999-12-28
35  <150> PRIOR APPLICATION NUMBER: 60/184,129
36  <151> PRIOR FILING DATE: 2000-02-22
38  <150> PRIOR APPLICATION NUMBER: 60/185,421
39  <151> PRIOR FILING DATE: 2000-02-28
41  <150> PRIOR APPLICATION NUMBER: 60/185,554
42  <151> PRIOR FILING DATE: 2000-02-28
44  <150> PRIOR APPLICATION NUMBER: 60/186,530
45  <151> PRIOR FILING DATE: 2000-03-02
47  <150> PRIOR APPLICATION NUMBER: 60/186,811
48  <151> PRIOR FILING DATE: 2000-03-03
50  <150> PRIOR APPLICATION NUMBER: 60/188,114
51  <151> PRIOR FILING DATE: 2000-03-09
53  <150> PRIOR APPLICATION NUMBER: 60/190,310
54  <151> PRIOR FILING DATE: 2000-03-17
56  <150> PRIOR APPLICATION NUMBER: 60/190,800
57  <151> PRIOR FILING DATE: 2000-03-21
59  <150> PRIOR APPLICATION NUMBER: 60/201,190
60  <151> PRIOR FILING DATE: 2000-05-02
62  <150> PRIOR APPLICATION NUMBER: 60/203,111
63  <151> PRIOR FILING DATE: 2000-05-08
65  <150> PRIOR APPLICATION NUMBER: 60/207,094
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RAW SEQUENCE LISTING   DATE: 12/01/2000
PATENT APPLICATION: US/09/714,449   TIME: 12:30:04

Input Set : A:\00431PHRM293.txt
Output Set: N:\CRF3\12012000\I714449.raw

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 66 <151> PRIOR FILING DATE: 2000-05-25
 68 <160> NUMBER OF SEQ ID NOS: 190
 70 <170> SOFTWARE: PatentIn version 3.0
 72 <210> SEQ ID NO: 1
 73 <211> LENGTH: 1182
 74 <212> TYPE: DNA
 75 <213> ORGANISM: H.Sapiens
 77 <400> SEQUENCE: 1
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 80 cctagctcct gctgatctag ttggggctcc agagtgggga ggagaaaggc actttgaaac     120
 82 ttctctgccc ttaccgtctt agccatcaaa ctctgagctg gagatagtga cgatgtgaca     180
 84 ggaactttcc ctgggcctct ctgggccaca attcctggcc gagagaaaga ggaggaatga     240
 86 ggtgagcacc ttcttcactc ctagggccat gtggtagagc tgcagtcgca cctccttctg     300
 88 ccaataggca tagatgagtg ggttgagcag ggagttgccc acgccgagca gccacaggta     360
 90 ccgttccagc actaggtaga ggtgacactc ctggcaggcc acctgcacaa tgccagtgat     420
 92 aaggaagggg gtccaggata gagcaaagct cccaatgaga acagacacag tacggagagc     480
 94 tttgaagtcg ctgggagtcc gtggggatcg ataacctcca gccatggctc ctgcatgttc     540
 96 catctttcga atctgctggc tgtgcatgaa ggcaatcttg agcatgtcgc agtagaagaa     600
 98 gacaaagagg agcatggctg ggaagaagcc aacgcaggag agggtcagca cgaagtgagg     660
100 gtgaaataca gcaaagaagc tgcactgccc tttgtaggca gtctgctgga acatgggggat    720
102 tccgagtggg aggaagccaa tgaggtaaga cactaaccac agcccggcaa tgcaggcccc     780
104 ggccacgaac ccactcatga tcttcaagta gcggaagggc tgcttgatgg caaggtacct     840
106 gtcaaggtg atcagcatga ccgtgaggac agaggcagct gcggaggaag tgacaaatgc      900
108 catccgcagg ctgcacaggg tcttctgtgt gggccgagaa gggctggaga gctggtctgt     960
110 gagtaggcca gagatggcca caccaatcaa ggtgtcagcc acagccagat tcaaggtgaa    1020
112 gcagagactg acaccatcat tcttgtggat caacagcagc acagccacag ccactagtgt    1080
114 gttagtagca atgatgaggg aggccaggac agcaaggatc actccaaatg agaaagatga    1140
116 ttccatgtct cgaagtggca ggacttcact taccagggca tg                      1182
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120 <211> LENGTH: 335
121 <212> TYPE: PRT
122 <213> ORGANISM: H.Sapiens
124 <400> SEQUENCE: 2
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127 1               5                   10                  15
129 Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
130                 20                  25                  30
132 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
133             35                  40                  45
135 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
136         50                  55                  60
138 Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
139 65                  70                  75                  80
141 Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
142                 85                  90                  95
144 Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
145             100                 105                 110
147 Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
148             115                 120                 125
```

```
RAW SEQUENCE LISTING                 DATE: 12/01/2000
PATENT APPLICATION:  US/09/714,449   TIME: 12:30:04

Input Set : A:\00431PHRM293.txt
Output Set: N:\CRF3\12012000\I714449.raw
```

```
150 Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
151     130                 135                 140
153 Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
154 145                 150                 155                 160
156 Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
157                 165                 170                 175
159 Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
160                 180                 185                 190
162 Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
163             195                 200                 205
165 Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
166     210                 215                 220
168 Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
169 225                 230                 235                 240
171 Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
172                 245                 250                 255
174 Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
175                 260                 265                 270
177 Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu
178             275                 280                 285
180 Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
181     290                 295                 300
183 Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu
184 305                 310                 315                 320
186 Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly
187                 325                 330                 335
189 <210> SEQ ID NO: 3
190 <211> LENGTH: 657
191 <212> TYPE: DNA
192 <213> ORGANISM: H.Sapiens
194 <400> SEQUENCE: 3
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197 gtgcacctgg agcgaggtga ggcagagcac cgccagcggc agcacgaagc ccacggcatg     120
199 gagcgtggcg gtgaaggctg cgaagcgcgg acgctcaggc tcgggcggca ggcgcagcga     180
201 acaggacgcg aaggcgctgc tgtagccaag ccacgaacag ccaagtgcag cgcctgagaa     240
203 ggccagcgac tgtccccagg cacagcccag cagcaggccg gcatagcgcg gtcgcaggcg     300
205 tccggcgtag cgcagtggga agcccactgc cagccactgg tctgcgctca gcgccgccac     360
207 gctcagcgcc gcgttggacg ccaggaaggt gtccaggaag ccaatgactt ggcatgcgcc     420
209 gggcgccgac ggtgtccgcc cgcgcatcac accgagcagc gtgaagggca tgtccagcgc     480
211 cgccagcagc aggtggccca gagacagatt caccagagcg acgcctgagg ctcgagtgcg     540
213 gagctcagcg ctgtaggcgc aacaaagcag caccagtgcg ttggatagca gcgccacggc     600
215 cagtaccatc accaggagac ccgccagcag cgcctcgccg gggcccatgg cgctagc       657
218 <210> SEQ ID NO: 4
219 <211> LENGTH: 217
220 <212> TYPE: PRT
221 <213> ORGANISM: H.Sapiens
223 <400> SEQUENCE: 4
225 Ser Ala Met Gly Pro Gly Glu Ala Leu Leu Ala Gly Leu Leu Val Met
226 1               5                   10                  15
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RAW SEQUENCE LISTING   DATE: 12/01/2000
PATENT APPLICATION: US/09/714,449   TIME: 12:30:04

Input Set : A:\00431PHRM293.txt
Output Set: N:\CRF3\12012000\I714449.raw

```
228 Val Leu Ala Val Ala Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Cys
229           20                  25                  30
231 Ala Tyr Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val
232           35                  40                  45
234 Asn Leu Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe
235         50                  55                  60
237 Thr Leu Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala
238 65                  70                  75                  80
240 Cys Gln Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala
241                 85                  90                  95
243 Leu Ser Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe
244           100                 105                 110
246 Pro Leu Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu
247         115                 120                 125
249 Leu Gly Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu
250       130                 135                 140
252 Gly Cys Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu
253 145                 150                 155                 160
255 Arg Leu Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala
256                 165                 170                 175
258 Thr Leu His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu
259               180                 185                 190
261 Thr Ser Leu Gln Val His Arg Val Ala Arg Arg His Cys Gln Arg Met
262         195                 200                 205
264 Asp Thr Val Thr Met Lys Ala Leu Ala
265 -     210                 215
267 <210> SEQ ID NO: 5
268 <211> LENGTH: 222
269 <212> TYPE: DNA
270 <213> ORGANISM: H.Sapiens
272 <400> SEQUENCE: 5
273 tgtgcaggtg tgatctccat tcctttgtac atccctcaca cgctgttcga atgggatttt    60
275 ggaaaggaaa tctgtgtatt ttggctcact actgactatc tgttatgtac agcatctgta   120
277 tataacattg tcctcatcag ctatgatcga tacctgtcag tctcaaatgc tgtaagtcga   180
279 acacattaat ttatccccct tagaagatta tgtaaatgta ta                      222
282 <210> SEQ ID NO: 6
283 <211> LENGTH: 73
284 <212> TYPE: PRT
285 <213> ORGANISM: H.Sapiens
287 <400> SEQUENCE: 6
289 Cys Ala Gly Val Ile Ser Ile Pro Leu Tyr Ile Pro His Thr Leu Phe
290 1           5                   10                  15
292 Glu Trp Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp
293           20                  25                  30
295 Tyr Leu Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr
296       35                  40                  45
298 Asp Arg Tyr Leu Ser Val Ser Asn Ala Val Ser Arg Thr His Phe Ile
299     50                  55                  60
301 Pro Leu Arg Arg Leu Cys Lys Cys Ile
```

```
            RAW SEQUENCE LISTING              DATE: 12/01/2000
            PATENT APPLICATION: US/09/714,449  TIME: 12:30:04

            Input Set : A:\00431PHRM293.txt
            Output Set: N:\CRF3\12012000\I714449.raw

302 65                      70
304 <210> SEQ ID NO: 7
305 <211> LENGTH: 507
306 <212> TYPE: DNA
307 <213> ORGANISM: H.Sapiens
309 <400> SEQUENCE: 7
310 gacgtcgaag caggtgatga tgcccagggc gtgcaccggg taggtgagat cggtgcgcgc      60
312 cagcggggac agggcggtca ggagcagcag ccaggtccct gcacacgcgg ccaccgcgta     120
314 acgacggcgg cgccagcgct tggagctgag cgggtacagg atccccagga agcgctccac     180
316 gctgatacag gtcatggtga ggatgctgga atacatgttt gcgtaaaagg ccacggtcac     240
318 cacgttgcaa agcagcaccc cgaataccca gtggtggcgg ttgcaatggt agtagatttg     300
320 gaaaggcaac acgctggcca gcatcaggtc cgtgacgctc aggttgatca tgaagatgac     360
322 cgacggggat ctggccccca tgccgccggca cagcaccac agagagaaga ggttgcccgg     420
324 gatgctgacc gccgccacca gcgagtacac cacgggcagg gccaccgcga tcgccgggtt     480
326 ccgcagcatc tgcagcgtcg cgttgtc                                         507
329 <210> SEQ ID NO: 8
330 <211> LENGTH: 169
331 <212> TYPE: PRT
332 <213> ORGANISM: H.Sapiens
334 <400> SEQUENCE: 8
336 Asp Asn Ala Thr Leu Gln Met Leu Arg Asn Pro Ala Ile Ala Val Ala
337 1               5                   10                  15
339 Leu Pro Val Val Tyr Ser Leu Val Ala Ala Val Ser Ile Pro Gly Asn
340                 20                  25                  30
342 Leu Phe Ser Leu Trp Val Leu Cys Arg Arg Met Gly Pro Arg Ser Pro
343             35                  40                  45
345 Ser Val Ile Phe Met Ile Asn Leu Ser Val Thr Asp Leu Met Leu Ala
346         50                  55                  60
348 Ser Val Leu Pro Phe Gln Ile Tyr Tyr His Cys Asn Arg His His Trp
349 65                  70                  75                  80
351 Val Phe Gly Val Leu Cys Asn Leu Val Val Thr Val Ala Phe Tyr Ala
352                 85                  90                  95
354 Asn Met Tyr Ser Ser Ile Leu Thr Met Thr Cys Ile Ser Val Glu Arg
355                 100                 105                 110
357 Phe Leu Gly Ile Leu Tyr Pro Leu Ser Ser Lys Arg Trp Arg Arg Arg
358             115                 120                 125
360 Arg Tyr Ala Val Ala Ala Cys Ala Gly Thr Trp Leu Leu Leu Leu Thr
361         130                 135                 140
363 Ala Leu Ser Pro Leu Ala Arg Thr Asp Leu Thr Tyr Pro Val His Ala
364 145                 150                 155                 160
366 Leu Gly Ile Ile Thr Cys Phe Asp Val
367                 165
369 <210> SEQ ID NO: 9
370 <211> LENGTH: 270
371 <212> TYPE: DNA
372 <213> ORGANISM: H.Sapiens
374 <400> SEQUENCE: 9
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377 gccgccaaca tcctactgtc ggggccgctc acgctgaaac tgtcccccgc gctctggttc     120
```

```
<210>  117
<211>  20
<212>  DNA
<213>  Artificial Sequence
```
see item 12 on Err. Summary sheet

```
<400>  117
acagccccaa agccaaacac                                          20
```

```
<210>  118
<211>  22
<212>  DNA
<213>  Artificial Sequence
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```
<400>  118
ccgcaggagc aatgaaaatc ag                                       22
```

```
<210>  119
<211>  19
<212>  DNA
<213>  Artificial Sequence
```

```
<400>  119
ctgaaagttg tcgctgacc                                           19
```

These errors exist in subsequent sequences, too.

Please edit.

        Input Set : A:\00431PHRM293.txt
        Output Set: N:\CRF3\12012000\I714449.raw

L:20 M:270 C: Current Application Number differs, Replaced Current Application No
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:615 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:666 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:976 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1020 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1023 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:2017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:4417 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:4417 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:4426 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:4426 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:4435 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:4435 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:4458 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:4458 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:4608 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:4608 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:4631 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:4631 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

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